

SEQUENCE LISTING

<110> Kobayashi, Masanori
Ueda, Yasuji
Hasegawa, Mamoru

<120> Methods of Producing a Viral Vector
Comprising a Membrane Protein That Binds To Sialic Acid As A
Component Of The Envelope Using Neuraminidase Derived From
Gram-Positive Bacteria

<130> 50026/050001

<150> PCT/JP03/11299
<151> 2003-09-04

<150> JP 2002-258576
<151> 2002-09-04

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1941
<212> DNA
<213> Micromonospora viridifaciens

<220>
<221> CDS
<222> (1) ... (1941)

<400> 1
atg act gcg aat ccg tac ctc cgc cgc ctg ccc cgg cgc cga gcc gtc 48
Met Thr Ala Asn Pro Tyr Leu Arg Arg Leu Pro Arg Arg Arg Ala Val
1 5 10 15

agc ttc ctg ctc gca cca gcg ctg gcg gcc gcc acg gtc gcc ggc gcg 96
Ser Phe Leu Leu Ala Pro Ala Leu Ala Ala Thr Val Ala Gly Ala
20 25 30

tcc ccc gca cag gcc atc gcc ggg gca ccc gtc cgg ccc ggc ggc gag 144
Ser Pro Ala Gln Ala Ile Ala Gly Ala Pro Val Pro Pro Gly Gly Glu
35 40 45

ccg ctc tac acg gag cag gac ctc gcc gtg aac ggc agg gag ggc ttt 192
Pro Leu Tyr Thr Glu Gln Asp Leu Ala Val Asn Gly Arg Glu Gly Phe
50 55 60

ccg aac tac cgc atc cca gcg ctg acc gtc acg ccc gac ggg gac ctg 240
Pro Asn Tyr Arg Ile Pro Ala Leu Thr Val Thr Pro Asp Gly Asp Leu
65 70 75 80

ctg gcc tcg tac gac ggc cgc ccg acc ggt atc gac gcg ccc ggc ccc 288
Leu Ala Ser Tyr Asp Gly Arg Pro Thr Gly Ile Asp Ala Pro Gly Pro
85 90 95

aac tcc atc ctc caa cgc cgc agc acc gac ggc ggc cg ^g acg tgg ggc		336	
Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Arg Thr Trp Gly			
100	105	110	
gag caa cag gtc gtc agc gcc ggc cag acc acc ggc cg ^g atc aag ggg		384	
Glu Gln Gln Val Val Ser Ala Gly Gln Thr Thr Ala Pro Ile Lys Gly			
115	120	125	
ttc tcc gac ccc agc tac ctt gtc gac cg ^g gaa acc ggg acc atc ttc		432	
Phe Ser Asp Pro Ser Tyr Leu Val Asp Arg Glu Thr Gly Thr Ile Phe			
130	135	140	
aac ttc cac gtc tac tcc cag cg ^g cag ggc ttc gcc ggc agc cg ^g ccc		480	
Asn Phe His Val Tyr Ser Gln Arg Gln Gly Phe Ala Gly Ser Arg Pro			
145	150	155	160
ggc acc gac ccg gca gac ccc aac gtg ctc cac gcc aac gtc ggc acc		528	
Gly Thr Asp Pro Ala Asp Pro Asn Val Leu His Ala Asn Val Ala Thr			
165	170	175	
tcg acc gac ggc ggt ctg acc tgg tcg cac cg ^g acc atc acg gcc gac		576	
Ser Thr Asp Gly Gly Leu Thr Trp Ser His Arg Thr Ile Thr Ala Asp			
180	185	190	
atc acc ccg gat ccg ggc tgg cg ^g agc cg ^g ttc gcc gcc tcc gg ^g gaa		624	
Ile Thr Pro Asp Pro Gly Trp Arg Ser Arg Phe Ala Ala Ser Gly Glu			
195	200	205	
ggc atc cag ctc cg ^g tat gga ccc cac gcc ggt cga ctc atc cag cag		672	
Gly Ile Gln Leu Arg Tyr Gly Pro His Ala Gly Arg Leu Ile Gln Gln			
210	215	220	
tac acg atc atc aac gct gcc ggc gcc ttc cag cg ^g gt ^g agc gt ^g tac		720	
Tyr Thr Ile Ile Asn Ala Ala Gly Ala Phe Gln Ala Val Ser Val Tyr			
225	230	235	240
agc gac gac cac gga agg acc tgg cg ^g gcc gg ^g gaa gcc gtc ggg gtc		768	
Ser Asp Asp His Gly Arg Thr Trp Arg Ala Gly Glu Ala Val Gly Val			
245	250	255	
ggc atg gac gag aac aag acc gt ^g gaa ctc tcc gat ggc cg ^g gtc ctg		816	
Gly Met Asp Glu Asn Lys Thr Val Glu Leu Ser Asp Gly Arg Val Leu			
260	265	270	
ctc aac agc cg ^g gac tcg gcc cg ^g agc gga tac cgt aag gt ^g gcc gtc		864	
Leu Asn Ser Arg Asp Ser Ala Arg Ser Gly Tyr Arg Lys Val Ala Val			
275	280	285	
tcc act gac ggc ggc cac agc tac ggc cg ^g gt ^g acc atc gac cg ^g gac		912	
Ser Thr Asp Gly Gly His Ser Tyr Gly Pro Val Thr Ile Asp Arg Asp			
290	295	300	
ctc ccc gac ccg acg aac aac gca tcg atc atc cg ^g gcc ttc cct gac		960	
Leu Pro Asp Pro Thr Asn Asn Ala Ser Ile Ile Arg Ala Phe Pro Asp			
305	310	315	320
gcc ccg gcc ggc tcc gcg cg ^g gcc aag gtc ctg ctc ttc tcc aac gcc		1008	

Ala Pro Ala Gly Ser Ala Arg Ala Lys Val Leu Leu Phe Ser Asn Ala			
325	330	335	
gcc agc cag acc tcg cgc agt cag ggc acc atc cgg atg tcc tgc gac			1056
Ala Ser Gln Thr Ser Arg Ser Gln Gly Thr Ile Arg Met Ser Cys Asp			
340	345	350	
gat ggc cag acc tgg ccg gtt tcg aag gtc ttc cag ccc ggc tcg atg			1104
Asp Gly Gln Thr Trp Pro Val Ser Lys Val Phe Gln Pro Gly Ser Met			
355	360	365	
tcg tac tcc acc ctg acc gca ctg ccc gac ggc acc tac ggg ctg ctg			1152
Ser Tyr Ser Thr Leu Thr Ala Leu Pro Asp Gly Thr Tyr Gly Leu Leu			
370	375	380	
tac gag ccg ggc acc ggc atc aga tac gcc aac ttc aac ctc gcc tgg			1200
Tyr Glu Pro Gly Thr Gly Ile Arg Tyr Ala Asn Phe Asn Leu Ala Trp			
385	390	395	400
ctg ggc ggc atc tgc gcg ccc ttc acg att ccg gat gtg gcg ctc gag			1248
Leu Gly Gly Ile Cys Ala Pro Phe Thr Ile Pro Asp Val Ala Leu Glu			
405	410	415	
ccg ggc cag cag gtc act gtt ccg gtg gcc gtc acg aac cag tcc ggt			1296
Pro Gly Gln Gln Val Thr Val Pro Val Ala Val Thr Asn Gln Ser Gly			
420	425	430	
atc gcg gta ccg aag ccg agc ctt cag ctc gac gca tcg ccg gac tgg			1344
Ile Ala Val Pro Lys Pro Ser Leu Gln Leu Asp Ala Ser Pro Asp Trp			
435	440	445	
cag gtt cag ggt tcc gtc gag ccc ctc atg ccc gga cgg cag gcc aag			1392
Gln Val Gln Gly Ser Val Glu Pro Leu Met Pro Gly Arg Gln Ala Lys			
450	455	460	
ggc cag gtg acc atc acg gtt ccc gcc ggc acc acc ccc ggt cgc tac			1440
Gly Gln Val Thr Ile Thr Val Pro Ala Gly Thr Thr Pro Gly Arg Tyr			
465	470	475	480
cgg gtc ggt gcg acg ctg cgc acc tcc gcg ggt aac gcg tcg acg acc			1488
Arg Val Gly Ala Thr Leu Arg Thr Ser Ala Gly Asn Ala Ser Thr Thr			
485	490	495	
ttc acg gtc acg gtt gga ctg ctc gac cag gcc cgg atg agc atc gcg			1536
Phe Thr Val Thr Val Gly Leu Leu Asp Gln Ala Arg Met Ser Ile Ala			
500	505	510	
gac gtc gac agc gag gag acc gcc cgc gaa gac ggg cgg gcg agc aac			1584
Asp Val Asp Ser Glu Glu Thr Ala Arg Glu Asp Gly Arg Ala Ser Asn			
515	520	525	
gtg atc gac ggc aac ccc tcg acg ttc tgg cac acc gaa tgg tcg cgt			1632
Val Ile Asp Gly Asn Pro Ser Thr Phe Trp His Thr Glu Trp Ser Arg			
530	535	540	
gcc gat gct cct ggc tac ccg cac cgc atc agc ctc gac ctc ggt ggc			1680
Ala Asp Ala Pro Gly Tyr Pro His Arg Ile Ser Leu Asp Leu Gly Gly			
545	550	555	560

acg cac acg atc agc ggc ctc cag tac acc cga cgg cag aac agc gcc	1728
Thr His Thr Ile Ser Gly Leu Gln Tyr Thr Arg Arg Gln Asn Ser Ala	
565 570 575	
aac gag cag gtc gcg gac tac gag atc tac acc agc ctg aac ggc acg	1776
Asn Glu Gln Val Ala Asp Tyr Glu Ile Tyr Thr Ser Leu Asn Gly Thr	
580 585 590	
acc tgg gat ggc ccg gtt gcc agc ggg cgc ttc acc acg tcc ctc gcg	1824
Thr Trp Asp Gly Pro Val Ala Ser Gly Arg Phe Thr Thr Ser Leu Ala	
595 600 605	
ccg cag cgc gcg gtc ttc ccg gcg cgg gac gcc agg tac atc cgg ttg	1872
Pro Gln Arg Ala Val Phe Pro Ala Arg Asp Ala Arg Tyr Ile Arg Leu	
610 615 620	
gtg gcc ctc agc gag cag acc ggg cac aag tac gcc gcg gtc gct gag	1920
Val Ala Leu Ser Glu Gln Thr Gly His Lys Tyr Ala Ala Val Ala Glu	
625 630 635 640	
ctg gag gtg gaa ggc cag cgc	1941
Leu Glu Val Glu Gly Gln Arg	
645	

<210> 2
 <211> 647
 <212> PRT
 <213> Micromonospora viridifaciens

<400> 2	
Met Thr Ala Asn Pro Tyr Leu Arg Arg Leu Pro Arg Arg Arg Ala Val	
1 5 10 15	
Ser Phe Leu Leu Ala Pro Ala Leu Ala Ala Ala Thr Val Ala Gly Ala	
20 25 30	
Ser Pro Ala Gln Ala Ile Ala Gly Ala Pro Val Pro Pro Gly Gly Glu	
35 40 45	
Pro Leu Tyr Thr Glu Gln Asp Leu Ala Val Asn Gly Arg Glu Gly Phe	
50 55 60	
Pro Asn Tyr Arg Ile Pro Ala Leu Thr Val Thr Pro Asp Gly Asp Leu	
65 70 75 80	
Leu Ala Ser Tyr Asp Gly Arg Pro Thr Gly Ile Asp Ala Pro Gly Pro	
85 90 95	
Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Arg Thr Trp Gly	
100 105 110	
Glu Gln Gln Val Val Ser Ala Gly Gln Thr Thr Ala Pro Ile Lys Gly	
115 120 125	
Phe Ser Asp Pro Ser Tyr Leu Val Asp Arg Glu Thr Gly Thr Ile Phe	
130 135 140	
Asn Phe His Val Tyr Ser Gln Arg Gln Gly Phe Ala Gly Ser Arg Pro	
145 150 155 160	
Gly Thr Asp Pro Ala Asp Pro Asn Val Leu His Ala Asn Val Ala Thr	
165 170 175	
Ser Thr Asp Gly Gly Leu Thr Trp Ser His Arg Thr Ile Thr Ala Asp	
180 185 190	
Ile Thr Pro Asp Pro Gly Trp Arg Ser Arg Phe Ala Ala Ser Gly Glu	
195 200 205	

Gly Ile Gln Leu Arg Tyr Gly Pro His Ala Gly Arg Leu Ile Gln Gln
 210 215 220
 Tyr Thr Ile Ile Asn Ala Ala Gly Ala Phe Gln Ala Val Ser Val Tyr
 225 230 235 240
 Ser Asp Asp His Gly Arg Thr Trp Arg Ala Gly Glu Ala Val Gly Val
 245 250 255
 Gly Met Asp Glu Asn Lys Thr Val Glu Leu Ser Asp Gly Arg Val Leu
 260 265 270
 Leu Asn Ser Arg Asp Ser Ala Arg Ser Gly Tyr Arg Lys Val Ala Val
 275 280 285
 Ser Thr Asp Gly Gly His Ser Tyr Gly Pro Val Thr Ile Asp Arg Asp
 290 295 300
 Leu Pro Asp Pro Thr Asn Asn Ala Ser Ile Ile Arg Ala Phe Pro Asp
 305 310 315 320
 Ala Pro Ala Gly Ser Ala Arg Ala Lys Val Leu Leu Phe Ser Asn Ala
 325 330 335
 Ala Ser Gln Thr Ser Arg Ser Gln Gly Thr Ile Arg Met Ser Cys Asp
 340 345 350
 Asp Gly Gln Thr Trp Pro Val Ser Lys Val Phe Gln Pro Gly Ser Met
 355 360 365
 Ser Tyr Ser Thr Leu Thr Ala Leu Pro Asp Gly Thr Tyr Gly Leu Leu
 370 375 380
 Tyr Glu Pro Gly Thr Gly Ile Arg Tyr Ala Asn Phe Asn Leu Ala Trp
 385 390 395 400
 Leu Gly Gly Ile Cys Ala Pro Phe Thr Ile Pro Asp Val Ala Leu Glu
 405 410 415
 Pro Gly Gln Gln Val Thr Val Pro Val Ala Val Thr Asn Gln Ser Gly
 420 425 430
 Ile Ala Val Pro Lys Pro Ser Leu Gln Leu Asp Ala Ser Pro Asp Trp
 435 440 445
 Gln Val Gln Gly Ser Val Glu Pro Leu Met Pro Gly Arg Gln Ala Lys
 450 455 460
 Gly Gln Val Thr Ile Thr Val Pro Ala Gly Thr Thr Pro Gly Arg Tyr
 465 470 475 480
 Arg Val Gly Ala Thr Leu Arg Thr Ser Ala Gly Asn Ala Ser Thr Thr
 485 490 495
 Phe Thr Val Thr Val Gly Leu Leu Asp Gln Ala Arg Met Ser Ile Ala
 500 505 510
 Asp Val Asp Ser Glu Glu Thr Ala Arg Glu Asp Gly Arg Ala Ser Asn
 515 520 525
 Val Ile Asp Gly Asn Pro Ser Thr Phe Trp His Thr Glu Trp Ser Arg
 530 535 540
 Ala Asp Ala Pro Gly Tyr Pro His Arg Ile Ser Leu Asp Leu Gly Gly
 545 550 555 560
 Thr His Thr Ile Ser Gly Leu Gln Tyr Thr Arg Arg Gln Asn Ser Ala
 565 570 575
 Asn Glu Gln Val Ala Asp Tyr Glu Ile Tyr Thr Ser Leu Asn Gly Thr
 580 585 590
 Thr Trp Asp Gly Pro Val Ala Ser Gly Arg Phe Thr Thr Ser Leu Ala
 595 600 605
 Pro Gln Arg Ala Val Phe Pro Ala Arg Asp Ala Arg Tyr Ile Arg Leu
 610 615 620
 Val Ala Leu Ser Glu Gln Thr Gly His Lys Tyr Ala Ala Val Ala Glu
 625 630 635 640
 Leu Glu Val Glu Gly Gln Arg
 645